

SUMMARIES

| Result | Score | Query | Match | Length | DB | ID | Description |
|--------|-------|-------|--------|--------|------------|----------------------|-------------|
| No. | | No. | | | | | |
| C 1 | 108 | 8..7 | 6914 | 8 | ZMA251453 | AJ251453 Zee mays | |
| C 2 | 102.4 | 7..9 | 9285 | 8 | ZM009989 | 009989 Zee mays D3 | |
| C 3 | 99 | 8..2 | 4695 | 8 | A69563 | A69563 Sequence: D3 | |
| C 4 | 98 | 7..9 | 4695 | 8 | ZMPHYT1 | AJ223470 Zee mays | |
| C 5 | 97 | 7..8 | 151802 | 8 | AF318188 | AF318188 Zee mays | |
| C 6 | 70.8 | 5..7 | 151802 | 8 | AF318188 | AF318188 Zee mays | |
| C 7 | 62.6 | 5..0 | 118866 | 6 | AC072357 | AC072357 Sequence | |
| C 8 | 62.2 | 5..0 | 266371 | 2 | AC030619 | AC030619 Nus muscu | |
| C 9 | 59 | 4..7 | 175931 | 17 | AC087093 | AC087093 Homo sapi | |
| C 10 | 56.4 | 4..7 | 321003 | 2 | BPXAL433 | BPX25176 Plasmodu | |
| C 11 | 57.8 | 4..6 | 954 | 3 | HS05253 | HS05253 Human Itgal | |
| C 12 | 57.8 | 4..6 | 1241 | 8 | MT07041 | X02893 Candida gla | |
| C 13 | 57.8 | 4..6 | 105374 | 2 | AC033308 | AC033308 Homo sapi | |
| C 14 | 57.2 | 4..6 | 170237 | 9 | AL137070 | AL137070 Human DNA | |
| C 15 | 50.8 | 4..6 | 1886 | 8 | AF305832 | AF305832 Zee mays | |
| C 16 | 50.4 | 4..6 | 67970 | 3 | PEXAL132 | AL031495 Zee mays | |
| C 17 | 50.4 | 4..5 | 169346 | 2 | AC004157 | AC004157 Plasmodu | |
| C 18 | 56 | 4..5 | 54745 | 3 | AC0844132 | AC0844132 Caenorhab | |
| C 19 | 55.6 | 4..5 | 15543 | 3 | AF194978 | AF194978 Bombyx mo | |
| C 20 | 55.6 | 4..5 | 15564 | 3 | AY048187 | AY048187 Bombyx mo | |
| C 21 | 55.6 | 4..5 | 178119 | 2 | AL137269 | AL137269 Homo sapi | |
| C 22 | 55.6 | 4..4 | 178189 | 9 | AC0733259 | AC0733259 Homo sapi | |
| C 23 | 54.2 | 4..3 | 156600 | 2 | AC004153 | AC004153 Plasmodu | |
| C 24 | 54.2 | 4..3 | 169794 | 3 | AC004688 | AC004688 Plasmodu | |
| C 25 | 54.2 | 4..3 | 180221 | 2 | AC007277 | AC007277 Homo sapi | |
| C 26 | 54 | 4..3 | 152878 | 3 | AC018D10A | AC018D10A Homo sapi | |
| C 27 | 54 | 4..3 | 170143 | 3 | AC048384 | AC048384 Homo sapi | |
| C 28 | 53.8 | 4..3 | 17443 | 3 | AC024806 | AC024806 Caenorhab | |
| C 29 | 53.8 | 4..3 | 150236 | 6 | HS101G31 | AL021877 Human DNA | |
| C 30 | 53.6 | 4..3 | 1141 | 6 | AX083744 | AX083744 Sequence | |
| C 31 | 53.4 | 4..3 | 35077 | 3 | CEY38H9A | AL021483 Caenorhab | |
| C 32 | 52.8 | 4..2 | 187873 | 3 | ACE068139 | ACE068139 Homo sapi | |
| C 33 | 52.6 | 4..2 | 85779 | 8 | SC0E11856 | AL031856 Saccharom | |
| C 34 | 52.6 | 4..2 | 113880 | 9 | PEXAL1394 | AL008970 Plasmodu | |
| C 35 | 52.4 | 4..2 | 143409 | 3 | AL162497 | AL162497 Human DNA | |
| C 36 | 52.4 | 4..2 | 161230 | 2 | AC011355 | AC011355 Homo sapi | |
| C 37 | 52.4 | 4..2 | 165578 | 2 | AC009678 | AC009678 Homo sapi | |
| C 38 | 52.4 | 4..2 | 331326 | 2 | AC006802 | AC006802 Caenorhab | |
| C 39 | 52.2 | 4..2 | 1141 | 6 | AX083744 | AX083744 Sequence | |
| C 40 | 52.2 | 4..2 | 110000 | 2 | AC036737.2 | AC036737.2 | |
| C 41 | 52.2 | 4..2 | 162125 | 2 | AC080105 | AC080105 Homo sapi | |
| C 42 | 51.8 | 4..2 | 143331 | 9 | AC091214 | AC091214 Homo sapi | |
| C 43 | 51.8 | 4..2 | 170781 | 9 | AC013473 | AC013473 Homo sapi | |
| C 44 | 51.6 | 4..2 | 182125 | 8 | AC090105 | AC090105 Homo sapi | |
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| RESULT | 7 | | |
| LOCUS | AX027357 | 13868 bp DNA | PAT 16-SEP-2000 |
| DEFINITION | Sequence 5 from Patent WO0037488. | | |
| ACCESSION | AX027357 | | |
| VERSION | AX027357.1 GI:10188332 | | |
| KEYWORDS | | | |
| SOURCE | Zea mays. | | |
| ORGANISM | Zea mays. | | |
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| Best Local Similarity | 55.0%; Pred. No. 0.0012; | | |
| Matches 191; Conservative | 0; Mismatches 144; Indels 12; Gaps | 3 | |
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| Oy | 367 | cctatacaatttttgtat-----tttagtaaatatagtaacagtttagttagt 416 | |
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| Db | 12205 | GCTGACCAATATTCACATATTAGCTATGACCTTTTATGTAATGCTCATATGCTTGCACAC | 12264 |
| Oy | 417 | tatttaagaactagctttttttaactagaacatttttagccaacctaagaatttagttagt 476 | |

| | | | |
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| Oy | 12265 | TATTGTTCACCACTAATTCACACACAGTTTTCATTCGAGTAACAA - GCCTCTCAG | 12323 |
| Oy | 477 | gtattcaaatcccccttaagccgctaagatgatgccttccttagaaccttaaccggcatcgttg | 536 |
| Db | 13224 | GCAATTCATAATGAGCCGGAATATTCCTCACAGCGCGTGAGAGATTCAATTAGTTGGGCTTGG | 12383 |
| Oy | 537 | agacacatttcatagaggtagtcigttaaagtcacgcgtcacagtata | 583 |
| Db | 12384 | GTTGGTCGTTGGTTGATGTCTCATCAATGAGTAACAACGACCGCCGA | 12430 |
| RESULT | 8 | | |
| LOCUS | AC020619/c | | |
| DEFINITION | Mus musculus clone RP23-5A1 strain C57BL/6J, WORKING DRAFT SEQUENCE, 8 unordered pieces. | | |
| ACCESSION | AC020619 | | |
| VERSION | AC020619.8 | GI:1520865 | |
| KEYWORDS | HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_FULLTOP; HTGS_ACTIVEFIN; | | |
| SOURCE | house mouse. | | |
| ORGANISM | Mus musculus | | |
| REFERENCE | Eukariota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. | | |
| AUTHORS | 1 (bases 1 to 26637) | | |
| TITLE | Genome Therapeutics Corporation Sequencing Center: Mouse Genome Sequence Data | | |
| JOURNAL | Unpublished | | |
| REFERENCE | 2 (bases 1 to 26637) | | |
| AUTHORS | Smith,D.R. | | |
| TITLE | Direct Submission | | |
| JOURNAL | Submitted (06-JAN-2000) Genome Therapeutics Corporation, 100 Beaver Street, Waltham, MA 02453, USA | | |
| COMMENT | On Aug 17, 2001 this sequence version replaced gi:14010801. | | |
| ----- Genome Center ----- | | | |
| Center: Genome Therapeutics Corporation | | | |
| Web site: http://www.genomecorp.com/ | | | |
| Contact: gtc-seqcenter@genomecorp.com | | | |
| Project Information | | | |
| Center project name: mg005 | | | |
| Summary Statistics | | | |
| Sequencing vector: N/A | | | |
| Chemistry: Dye-terminator Big Dye; 100% of reads | | | |
| Assembly program: Phrap; version 990315 | | | |
| Consensus quality: 253434 bases at least Q40 | | | |
| Consensus quality: 255981 bases at least Q30 | | | |
| Consensus quality: 257373 bases at least Q20 | | | |
| Insert size: 265770; sum-of-contigs | | | |
| Quality coverage: 6.2x in Q20 bases; sum-of-contigs | | | |
| ----- NOTE: This is a 'working draft' sequence. It currently consists of 8 contigs. The true order of the pieces is as known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved. ----- | | | |
| * | 1 | 1229: contig of 1229 bp in length | |
| * | 1230 | 1329: gap of unknown length | |
| * | 1303 | 2533: contig of 1204 bp in length | |
| * | 2534 | 2633: gap of unknown length | |
| * | 2634 | 12786: contig of 10153 bp in length | |
| * | 12787 | 12886: gap of unknown length | |
| * | 12887 | 26730: contig of 13844 bp in length | |
| * | 26731 | 26830: gap of unknown length | |
| * | 26831 | 48101: contig of 21271 bp in length | |
| * | 48102 | 48201: gap of unknown length | |
| * | 48202 | 78531: contig of 30330 bp in length | |
| * | 78532 | 78631: gap of unknown length | |
| * | 78632 | 149349: contig of 70718 bp in length | |

| | | | |
|----|---------------|------------------------------|-----------------------------|
| FT | repeat_region | 7666. .8187 | /rpt_family="SINE/Alu" |
| FT | | /rpt_unit=AluY | |
| FT | repeat_region | complement(8533. .9034) | |
| FT | | /rpt_family="LINE/L1" | |
| FT | repeat_region | 9654. .9993 | /rpt_unit=L1mD3 |
| FT | | /rpt_family="SINE/MIR" | |
| FT | | /rpt_unit=MIR | |
| FT | repeat_region | 10289. .10397 | /rpt_family="LINE/L2" |
| FT | | /rpt_unit=L2 | |
| FT | repeat_region | complement(10551. .10861) | |
| FT | | /rpt_family="SINE/Alu" | |
| FT | repeat_region | complement(10947. .11117) | /rpt_unit=AluCb |
| FT | | /rpt_family="SINE/MIR" | |
| FT | repeat_region | 11164. .11232 | /rpt_unit=MIR |
| FT | | /rpt_family="LINE/L2" | |
| FT | repeat_region | complement(12045. .12215) | |
| FT | | /rpt_family="SINE/MIR" | |
| FT | repeat_region | complement(12652. .13133) | /rpt_unit=MIR |
| FT | | /rpt_family="LINE/L1" | |
| FT | repeat_region | complement(13146. .13447) | /rpt_unit=L1PA16 |
| FT | | /rpt_family="SINE/Alu" | |
| FT | repeat_region | complement(13448. .13593) | /rpt_unit=AluCo |
| FT | | /rpt_family="LINE/L1" | |
| FT | repeat_region | 13604. .13724 | /rpt_unit=L1PA16 |
| FT | | /rpt_family="LINE/L1" | |
| FT | repeat_region | 14467. .14539 | /rpt_unit=L1mE1 |
| FT | | /rpt_family="LINE/Other" | |
| FT | repeat_region | 14670. .14709 | /rpt_unit=HAL1 |
| FT | | /rpt_family="Low_complexity" | |
| FT | repeat_region | 16700. .16843 | /rpt_unit=Ar_rich |
| FT | | /rpt_family="SINE/MIR" | |
| FT | repeat_region | complement(17102. .17273) | /rpt_unit=MIR |
| FT | | /rpt_family="SINE/MIR" | |
| FT | repeat_region | complement(17502. .17804) | /rpt_family="SINE/Alu" |
| FT | | /rpt_unit=AluY | |
| FT | repeat_region | complement(17944. .18048) | /rpt_family="SINE/MIR" |
| FT | | /rpt_unit=MIR | |
| FT | repeat_region | 18206. .18514 | /rpt_family="LINE/L2" |
| FT | | /rpt_unit=L2 | |
| FT | repeat_region | 18737. .18763 | /rpt_family="Simple_repeat" |
| FT | | /rpt_unit="(A)n | |
| FT | repeat_region | 19870. .19945 | /rpt_family="LINE/L1" |
| FT | | /rpt_unit=L1mA7 | |
| FT | repeat_region | 20341. .20438 | /rpt_unit=L2 |
| FT | | complement(20572. .20598) | |
| FT | repeat_region | /rpt_family="DNA/MER1_type" | |
| FT | | complement(20599. .20898) | |
| FT | repeat_region | /rpt_family="SINE/Alu" | |
| FT | | /rpt_unit=AluCo | |
| FT | repeat_region | complement(20899. .21074) | |

[illegible]

TITLE
JOURNAL
REFERENCE
AUTHORS

Homo sapiens, clone RP11-6D2
2 (bases 1 to 105574)
Britten, B., Linton, L., Nusbaum, C., Lander, E., Allen, N., Anderson, M., Bateman, J., Barta, N., Beckert, R., Boguslavsky, L., Bouknight, B., Brown, A., Castle, A., Colangelo, M., Collins, S., Collymore, A., Cooke, P., DeRubeis, K., Dewar, K., Domino, M., Donelan, L., Doyle, M., Ferreira, P., Fitzhugh, W., Forrest, C., Funke, R., Gege, D., Galagan, J., Gardina, S., Grant, G., Haggis, B., Hefford, A., Horton, L., Howard, J., Johnson, R., Jones, C., Kann, L., Karas, A., Kiehn, J., Lebeck, J., Liu, C., Locke, K., MacDonald, P., Marcis, N., McKean, P., McGurk, A., McKernan, K., McLaughlin, J., Meldrum, J., Morrow, J., Naylor, J., Norman, C. H., O'Connor, T., O'Donnell, P., Peterson, K., Pollara, V., Riley, R., Roy, A., Santos, R., Severy, P., Stange, P., Stojanovic, N., Subramanian, A., Talamas, J., Testa, S., Tittell, A., Vassiliou, H., Vo, A., Wheeler, J., Wu, X., Wyman, D., Ye, W., Zimmer, A. and Zody, M.
Direct Submission
Submitted (06-NOV-1999) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA
On Jul 13, 2000 this sequence version replaced g1:5289194.
All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
<http://ftp.genome.washington.edu/RM/RepeatMasker.html>.

Genome Center

Center: Whitehead Institute/ MIT Center for Genome Research

Center code: WIBR

Web site: <http://www.seq.wi.mit.edu>

Contact: sequence.submissions@genome.wi.mit.edu

Project information

Center project name: L2882

Center clone name: 6_D_2

NOTE: This record contains 112 individual
* sequencing reads that have not been assembled into
* contigs. Runs of N are used to separate the reads
* and the order in which they appear is completely
* arbitrary. Low-pass sequence sampling is useful for
* identifying clones that may be gene-rich and allows
* overlap relationships among clones to be deduced.
* However, it should not be assumed that this clone
* will be sequenced to completion. In the event that
* the record is updated, the accession number will
* be preserved.

1 875: contig of 875 bp in length
* 876 975: gap of 100 bp
* 976 1849: contig of 874 bp in length
* 1850 1949: gap of 100 bp
* 1950 2811: contig of 862 bp in length
* 2812 2911: gap of 100 bp
* 2912 3742: contig of 831 bp in length
* 3743 3842: gap of 100 bp
* 3843 4717: contig of 875 bp in length
* 4718 4817: gap of 100 bp
* 4818 5413: contig of 596 bp in length
* 5414 5513: gap of 100 bp
* 5514 6398: contig of 885 bp in length
* 6399 6498: gap of 100 bp
* 6499 7384: contig of 886 bp in length
* 7385 7484: gap of 100 bp
* 7485 8357: contig of 873 bp in length
* 8358 8457: gap of 100 bp
* 8458 9306: contig of 849 bp in length
* 9307 9406: gap of 100 bp
* 9407 10257: contig of 851 bp in length
* 10258 10357: gap of 100 bp
* 10358 11213: contig of 856 bp in length
* 11214 11313: gap of 100 bp
* 11314 12162: contig of 849 bp in length
* 12163 12262: gap of 100 bp
* 12263 13138: contig of 876 bp in length
* 13139 13238: gap of 100 bp
* 13239 14081: contig of 843 bp in length

14082 14181: gap of 100 bp
* 14182 15085: contig of 904 bp in length
* 15086 15185: gap of 100 bp
* 15186 16034: contig of 849 bp in length
* 16035 16134: gap of 100 bp
* 16135 16996: contig of 862 bp in length
* 16997 17096: gap of 100 bp
* 17097 17938: contig of 842 bp in length
* 17939 18038: gap of 100 bp
* 18039 18902: contig of 864 bp in length
* 18903 19002: gap of 100 bp
* 19003 19838: contig of 836 bp in length
* 19839 19938: gap of 100 bp
* 19939 20820: contig of 882 bp in length
* 20821 20920: gap of 100 bp
* 20921 21793: contig of 873 bp in length
* 21794 21893: gap of 100 bp
* 21894 22781: contig of 888 bp in length
* 22782 22881: gap of 100 bp
* 22882 23730: contig of 849 bp in length
* 23731 23830: gap of 100 bp
* 23831 24494: contig of 664 bp in length
* 24495 24594: gap of 100 bp
* 24595 25452: contig of 858 bp in length
* 25453 25552: gap of 100 bp
* 25553 26413: contig of 861 bp in length
* 26414 26513: gap of 100 bp
* 26514 27371: contig of 858 bp in length
* 27372 27471: gap of 100 bp
* 27472 28398: contig of 927 bp in length
* 28399 28498: gap of 100 bp
* 28499 29355: contig of 857 bp in length
* 29356 29455: gap of 100 bp
* 29456 30343: contig of 888 bp in length
* 30344 30443: gap of 100 bp
* 30444 31343: contig of 900 bp in length
* 31344 31443: gap of 100 bp
* 31444 32303: contig of 860 bp in length
* 32304 32403: gap of 100 bp
* 32404 33294: contig of 891 bp in length
* 33295 33394: gap of 100 bp
* 33395 34263: contig of 869 bp in length
* 34264 34363: gap of 100 bp
* 34364 35268: contig of 935 bp in length
* 35269 35368: gap of 100 bp
* 35369 36267: contig of 869 bp in length
* 36268 36367: gap of 100 bp
* 36368 37216: contig of 849 bp in length
* 37217 37316: gap of 100 bp
* 37317 38168: contig of 852 bp in length
* 38169 38268: gap of 100 bp
* 38269 38903: contig of 635 bp in length
* 38904 39003: gap of 100 bp
* 39004 39880: contig of 877 bp in length
* 39881 39980: gap of 100 bp
* 39981 40850: contig of 870 bp in length
* 40851 40950: gap of 100 bp
* 40951 41839: contig of 889 bp in length
* 41840 41939: gap of 100 bp
* 41940 42805: contig of 867 bp in length
* 42807 42906: gap of 100 bp
* 42907 43626: contig of 720 bp in length
* 43627 43726: gap of 100 bp
* 43727 44580: contig of 854 bp in length
* 44581 44680: gap of 100 bp
* 44681 45529: contig of 849 bp in length
* 45530 45629: gap of 100 bp
* 45630 46365: contig of 736 bp in length
* 46366 46465: gap of 100 bp
* 46466 47383: contig of 918 bp in length
* 47384 47483: gap of 100 bp
* 47484 48358: contig of 875 bp in length
* 48359 48458: gap of 100 bp


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Query Match      4.6%; Score 57.2; DB 9; Length 70237;
Best Local Similarity 49.0%; Pred. No. 0.022;
Matches 237; Conservative 0; Mismatches 243; Indels 4; Gaps 3;

QY 5 taccataaagttggaatatacatatccattcaacataaagaacccaattaaat 64
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 98104 TATATATATATATATATATATATATATATATATATATATATATATAT 98163
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 65 aacataaataaataacattatcacccgtacaggaagagagacatcaacttgctt 124
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 98164 AATATATATATATATATATATATATATATATATATATATATATATAT 98222
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 125 atgcatttaaacaccctcgaaccatcagcagtggttgataggcttaactgata 184
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 98223 ATATATATATATATATATATATATATATATATATATATATATATAT 98282
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 185 tctgtcttaatactagcacacacacacacacacacacacacacacacacac 244
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 98283 TATATATATATATATATATATATATATATATATATATATATATATAT 98342
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 245 tctgtcttaatactagcacacacacacacacacacacacacacacacacac 304
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 98343 TATATATATATATATATATATATATATATATATATATATATATATAT 98402
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 305 tgaatctggaatgacacacacacacacacacacacacacacacacacacac 364
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 98403 ATATATATATATATATATATATATATATATATATATATATATATAT 98460
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 365 caccctacacatctagctat-ctttagtaattagtaattagctagctagctat 423
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 98461 TATATATATATATATATATATATATATATATATATATATATATATAT 98520
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 424 aagcagaacttttcttagcgaactttttagcgaacacacacacacacacacac 483
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 98521 ATTATATATATATATATATATATATATATATATATATATATATATAT 98580
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 484 aata 487
    |||||
Db 98581 TATA 98584
    |||||

RESULT 15
AF305892 1986 bp mRNA PLN 03-FEB-2001
LOCUS AF305892
DEFINITION Zea mays microtubule-binding protein TANGLED1 mRNA, complete cds.
ACCESSION AF305892
VERSION AF305892.1 GI:11228985
KEYWORDS
SOURCE
ORGANISM Zea mays.
Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
Magnoliophyta; Liliopsida; Poales; Poaceae; PACC clade;
Panicoideae; Andropogoneae; Zea.
REFERENCE
AUTHORS Smith, L.G., Gertula, S.M., Han, S. and Levy, J.
TITLE TANGLED1. A microtubule binding protein required for the spatial
JOURNAL J. Cell Biol. 152 (1), 231-236 (2001)
PUBMED 11149933
REFERENCE 2 (bases 1 to 1986)
AUTHORS Smith, L.G.
TITLE Direct Submission
JOURNAL Submitted (15-SEP-2000) Biology, U.C.S.D., 9500 Gilman Drive, La
Jolla, CA 92093-0116, USA
FEATURES
source
Location/Qualifiers
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/organism="Zea mays"
/db_xref="taxon:4577"
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81..1241
/codon_start=1
/product="microtubule-binding protein TANGLED1"
CDS

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/protein_id="AAC33234.1"
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VGGESAKORRRMSLPAMLGETVLEIVQASOFARDIVTAAGATREPRTPKPAPTTK
PAGSEPPLRARBARERKOSHRGGAATRGADATPPSRVRSRIGRPVSPVAVGRPS
VSANVSPSKNRPMAKVMPPNPPTPASATDPCATPPSKKKRRLTKRSPVAAR
ORPHKFLVKSPPSALGSKLMDHGKALPARPAVSPPPVNRQASPAKTPRCSFSPRL
ATRLMSPIKALSLGRSRDSGVYGGGCPMSGLKQRPVSTVTVTSKISR"
BASE COUNT 425 a 577 c 599 g 382 t
ORIGIN

```

```

Query Match      4.6%; Score 56.8; DB 8; Length 1986;
Best Local Similarity 68.0%; Pred. No. 0.02;
Matches 123; Conservative 0; Mismatches 53; Indels 5; Gaps 3;

QY 308 tgttgaatgacataagtaagtaagtaagtaagtaagtaagtaagtaagtaag 367
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1738 TCTTGAATGCACT-CACTATATAGTTCCTTAATATAGTCAACATCCANNAC 1796
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 368 cctatcaattatagttattttagtaattagtaattagttattttagtaagc 427
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1797 TCTATTTGATAGTTCACTATAGTTATTTTATCAAA--TTGCTATAGTTGCTGC 1853
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 428 tagctttttttagtaagaaatttttagcgaacacacacacacacacacacacac 487
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1854 TACCTAATTCCTCTAGCAATTGG-TAGCCACACTACATATAGCTAGTGAATCAACA 1912
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 488 c 488
    |||||
Db 1913 C 1913
    |||||

```

Search completed: December 20, 2001, 12:26:47
 Job time: 8596 sec

| | | | |
|-------------|---|--|-----|
| Oy | 423 | tactctagcgttttctaagaatttttagccaaataatglttttggtatcc | 482 |
| Db | 368 | AA | 309 |
| Oy | 483 | aataaccacgaagccgtaagtgaicgtcttccttagaatccaagtgaggaca | 542 |
| Db | 308 | AA | 249 |
| Oy | 543 | catttcaagatgtacctgtttaagtcacgcylgaataaataattcccacgcg | 602 |
| Db | 248 | AA | 189 |
| Oy | 603 | ttcttaagcaaacgccagtcgaatcatatttacaactagcggtctgaagaaa | 662 |
| Db | 188 | AA | 129 |
| Oy | 663 | ccccgtgcataagatatcttaacacgcgttggtaacaactgccttgaaaa | 722 |
| Db | 128 | AA | 69 |
| Oy | 723 | tactactagccctagctgactgacgcggcgtaaaaaacgtacgtgaaaa | 774 |
| Db | 68 | AA | 17 |
| RESULT | 3 | | |
| AATF8237/c | | | |
| ID | AATF8237 | standard; DNA; 936 BP. | |
| AC | AATF8237; | | |
| XX | | | |
| DT | 24-APR-2001 | (first entry) | |
| De | Oligonucleotide D1954. | | |
| KM | Electron-transfer group; ETW; mismatch; genotyping; | | |
| KX | gene expression; ss. | | |
| OS | Synthetic. | | |
| XX | | | |
| PN | MO200107665-A2. | | |
| PD | | | |
| PE | 01-FEB-2001. | | |
| PF | 26-JUL-2000; 2000MO-US20476. | | |
| PR | 26-JUL-1989; 99HS-0145695. | | |
| PR | 17-MAR-2000; 2000US-0190259. | | |
| PA | (CLIN-) CLINICAL MICRO SENSORS INC. | | |
| PI | UmeK RM; | | |
| DR | UPI: 2001-159728/16. | | |
| PT | Nucleic acids containing electron-transfer group, useful as labels in hybridization assays, e.g. for genotyping, allowing repeat analyses on a single surface | | |
| PS | Example 6; Page 127; 159pp: English. | | |
| CC | The present invention relates to a composition comprising two nucleic acids each containing an electron-transfer group (ETW) having different redox potentials. The invention is used for electronic detection of nucleic acids, especially of substitutions (mismatches) and single-nucleotide polymorphisms, e.g. for genotyping, monitoring gene expression. | | |
| XQ | Sequence 936 BP; 5 A; 142 C; 7 G; 6 T; 776 other; | | |
| Query Match | 12.9%; Score 161.2; DB 22; Length 936; | | |

[illegible]

Best Local Similarity 1.2%; Pred. No. 8.7e-30;
Matches 8; Conservative 466; Mismatches 212; Indels 0; Gaps 0;

```

QY 1 atcgtaactaaagtgtgataatatacattacattacaaatgaacaaatatt 60
   ||| : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 96 wncwcnwcnwcnwcnwcnwcnwcnwcnwcnwcnwcnwcnwcnwcnwcnw 155
   : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 61 taaaactaaataaaacattatcacgcgtacagagagagacatcgtctatag 120
   : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 156 wcnwcnwcnwcnwcnwcnwcnwcnwcnwcnwcnwcnwcnwcnwcnw 215
   : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 121 tttaatgatttaaacacccctcgaaacacacagcagtggttagagtttaact 180
   : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 216 wcnwcnwcnwcnwcnwcnwcnwcnwcnwcnwcnwcnwcnwcnwcnw 275
   : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 181 aatatctgtctttaactagacacaaactgataatactcttcgaacacatgtatatt 240
   : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 276 wcnwcnwcnwcnwcnwcnwcnwcnwcnwcnwcnwcnwcnwcnwcnw 335
   : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 241 ctattgttgacttaataactaaatccaaagatagtagagatgtagatagatt 300
   : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 336 wcnwcnwcnwcnwcnwcnwcnwcnwcnwcnwcnwcnwcnwcnwcnw 395
   : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 301 aagtgatgtttgaatgacacagacaaatagtagtaataatagttgagacatt 360
   | : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 396 awnwcnwcnwcnwcnwcnwcnwcnwcnwcnwcnwcnwcnwcnwcnwcnw 455
   : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 361 caaacacccatacatatagttatttttagtaataatagttagttagttatt 420
   : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 456 wcnwcnwcnwcnwcnwcnwcnwcnwcnwcnwcnwcnwcnwcnwcnw 515
   : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 421 tataagcagcttttttaactagcaatttttaagcacaatacattagtttagtatt 480
   : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 516 wcnwcnwcnwcnwcnwcnwcnwcnwcnwcnwcnwcnwcnwcnwcnw 575
   : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 481 tcaaatccccaaacgcgttaagtagtcttctttagaatcttaacgcatctgagac 540
   : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 576 wcnwcnwcnwcnwcnwcnwcnwcnwcnwcnwcnwcnwcnwcnwcnw 635
   : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 541 aacatttcaatagtgtagctttaaagtcacgcgtcagtgataataatttcaacatcg 600
   : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 636 wcnwcnwcnwcnwcnwcnwcnwcnwcnwcnwcnwcnwcnwcnwcnw 695
   : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 601 gtcttctaagcaaacgcgcgtctaatgataattacactagcggtctgctaagaataac 660
   : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 696 wcnwcnwcnwcnwcnwcnwcnwcnwcnwcnwcnwcnwcnwcnwcnw 755
   : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 661 cgcgcgtgctaagaatttacaata 686
   : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 756 wcnwcnwcnwcnwcnwcnwcnwcnwcnwcnwcnwcnwcnwcnwcnw 781
   : : : : : : : : : : : : : : : : : : : : : : : : : :

```

RESULT 9

AAFS8257
ID AAFS8257 standard; DNA; 936 BP.

AC AAFS8257;

DT 24-APR-2001 (first entry)

XX Oligonucleotide D1954.

XX electron-transfer group; ETM; mismatch; genotyping;

KW gene expression; ss.

XX Synthetic.

XX PN MO20010765-A2.

XX PD 01-FEB-2001.

XX PF 26-JUL-2000; 2000MO-US20476.

PR 26-JUL-1999; 9905-0145695.
PR 17-MAR-2000; 2000US-0190259.

XX (CLIN-) CLINICAL MICRO SENSORS INC.

PI umek RM;

DR WPI; 2001-159728/16.

XX Nucleic acids containing electron-transfer group, useful as labels in

PT hybridization assays, e.g. for genotyping, allowing repeat analyses on

PS a single surface -

XX Example 6; Page 127; 159pp; English.

CC The present invention relates to a composition comprising two nucleic

CC acids each containing an electron-transfer group (ETM) having

CC different redox potentials. The invention is used for electronic

CC detection of nucleic acids, especially of substitutions (mismatches)

CC and single-nucleotide polymorphisms, e.g. for genotyping,

XX monitoring gene expression.

XX Sequence 936 BP; 5 A; 142 C; 7 G; 6 T; 776 other;

Query Match 12.9%; Score 160.4; DB 22; Length 936;

Best Local Similarity 1.2%; Pred. No. 8.7e-30;

Matches 8; Conservative 466; Mismatches 212; Indels 0; Gaps 0;

```

QY 1 atcgtaactaaagtgtgataatatacattacattacaaatgaacaaatatt 60
   ||| : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 96 wcnwcnwcnwcnwcnwcnwcnwcnwcnwcnwcnwcnwcnwcnwcnw 155
   : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 61 taaaactaaataaaacattatcacgcgtacagagagagacatcgtctatag 120
   : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 156 wcnwcnwcnwcnwcnwcnwcnwcnwcnwcnwcnwcnwcnwcnwcnw 215
   : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 121 tttaatgatttaaacacccctcgaaacacacagcagtggttagagtttaact 180
   : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 216 wcnwcnwcnwcnwcnwcnwcnwcnwcnwcnwcnwcnwcnwcnwcnw 275
   : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 181 aatatctgtctttaactagacacaaactgataatactcttcgaacacatgtatatt 240
   : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 276 wcnwcnwcnwcnwcnwcnwcnwcnwcnwcnwcnwcnwcnwcnwcnw 335
   : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 241 ctattgttgacttaataactaaatccaaagatagtagagatgtagatagatt 300
   : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 336 wcnwcnwcnwcnwcnwcnwcnwcnwcnwcnwcnwcnwcnwcnwcnw 395
   : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 301 aagtgatgtttgaatgacacagacaaatagtagtaataatagttgagacatt 360
   | : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 396 awnwcnwcnwcnwcnwcnwcnwcnwcnwcnwcnwcnwcnwcnwcnwcnw 455
   : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 361 caaacacccatacatatagttatttttagtaataatagttagtttagttatt 420
   : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 456 wcnwcnwcnwcnwcnwcnwcnwcnwcnwcnwcnwcnwcnwcnwcnw 515
   : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 421 tataagcagcttttttaactagcaatttttaagcacaatacattagtttagtatt 480
   : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 516 wcnwcnwcnwcnwcnwcnwcnwcnwcnwcnwcnwcnwcnwcnwcnw 575
   : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 481 tcaaatccccaaacgcgttaagtagtcttctttagaatcttaacgcatctgagac 540
   : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 576 wcnwcnwcnwcnwcnwcnwcnwcnwcnwcnwcnwcnwcnwcnwcnw 635
   : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 541 aacatttcaatagtgtagctttaaagtcacgcgtcagtgataataatttcaacatcg 600
   : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 636 wcnwcnwcnwcnwcnwcnwcnwcnwcnwcnwcnwcnwcnwcnwcnw 695
   : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 601 gtcttctaagcaaacgcgcgtctaatgataattacactagcggtctgctaagaataac 660
   : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 696 wcnwcnwcnwcnwcnwcnwcnwcnwcnwcnwcnwcnwcnwcnwcnw 755
   : : : : : : : : : : : : : : : : : : : : : : : : : :

```

OY 661 cgcccgtaagaatattaccta 686
 DB 756 www. 781

RESULT 10

AAFS8259
 ID AAF58259 standard; DNA; 936 BP.

AC AAF58259;

DR 24-APR-2001 (first entry)

DE Oligonucleotide D2004.

Electron-transfer group; ETM; mismatch; genotyping;
 gene expression; ss.

XX Synthetic.

PN WO200107665-A2.

PD 01-FEB-2001.

PF 26-JUL-2000; 2000MO-US20476.

PR 26-JUL-1999; 99US-0145695.

PR 17-MAR-2000; 2000US-0190259.

PA (CLIN-) CLINICAL MICRO SENSORS INC.

PI Umek RM;

DR WPI: 2001-159728/16.

PT Nucleic acids containing electron-transfer group, useful as labels in
 hybridization assays, e.g. for genotyping, allowing repeat analyses on
 a single surface

XX Example 6; Page 128; 159pp; English.

CC The present invention relates to a composition comprising two nucleic
 acids each containing an electron-transfer group (ETM) having
 different redox potentials. The invention is used for electronic
 detection of nucleic acids, especially of substitutions (mismatches)
 and single-nucleotide polymorphisms, e.g. for genotyping,
 monitoring gene expression.

CC Sequence 936 BP; 6 A; 138 C; 8 G; 8 T; 776 other;

Query Match 12.9%; Score 160.4; DB 22; Length 936;

Best Local Similarity 1.2%; Pred. No. 8.7e-30;

Matches 8; Conservative 466; Mismatches 212; Indels 0; Gaps 0;

OY 1 atcgataaagttgataatcatcattcaactaactaagaacacattatc 60

DB 96 www. 155

OY 61 taataaactaataaactctacacgtagagagagagacatctattag 120

DB 156 www. 215

OY 121 tttaatgatttaaacacccctcgaaacatcagcagtggtgatagttaactgatact 180

DB 216 www. 275

OY 161 aatctgtctttaactagcaccaactgataataactttcgaaacatgttatat 240

DB 276 www. 335

OY 241 ctatgtgacttaactaactaataacaaagatatagtagagatgtgataagatt 300

DB 336 www. 395
 OY 301 aagtgatgtttgaatgcactagagcctaagtagtagtaaatagctggagacatt 360
 DB 396 www. 455
 OY 361 caaacacccataatattagttatttttagtaaatagtagtagtagtatt 420
 DB 456 www. 515
 OY 421 tataagcagcttttttactagcaatttttagccaactaacaattagtttagtat 480
 DB 516 www. 575
 OY 481 taataacccctaagcgttaagtgatgctcttctagaacttaacgcatgtggagac 540
 DB 576 www. 635
 OY 541 aacatttcatagtgtagctttaagtcacgcgtcagtgataataatttcacatgcg 600
 DB 636 www. 695
 OY 601 gttccttaagcaaacgcagtcgaatgatatattacacagcggctgctaagaataac 660
 DB 696 www. 755
 OY 661 cgcccgtaagaatattaccta 686
 DB 756 www. 781

RESULT 11

AAFS8262
 ID AAF58262 standard; DNA; 936 BP.

AC AAF58262;

DR 24-APR-2001 (first entry)

DE Oligonucleotide D2007.

Electron-transfer group; ETM; mismatch; genotyping;
 gene expression; ss.

XX Synthetic.

PN WO200107665-A2.

PD 01-FEB-2001.

PF 26-JUL-2000; 2000MO-US20476.

PR 26-JUL-1999; 99US-0145695.

PR 17-MAR-2000; 2000US-0190259.

PA (CLIN-) CLINICAL MICRO SENSORS INC.

PI Umek RM;

DR WPI: 2001-159728/16.

PT Nucleic acids containing electron-transfer group, useful as labels in
 hybridization assays, e.g. for genotyping, allowing repeat analyses on
 a single surface

XX Example 6; Page 128; 159pp; English.

CC The present invention relates to a composition comprising two nucleic
 acids each containing an electron-transfer group (ETM) having
 different redox potentials. The invention is used for electronic
 detection of nucleic acids, especially of substitutions (mismatches)
 and single-nucleotide polymorphisms, e.g. for genotyping,
 monitoring gene expression.

XX Sequence 936 BP; 5 A; 139 C; 10 G; 6 T; 776 other;
SQ

Query Match 12.9%; Score 160.4; DB 22; Length 936;
Best Local Similarity 1.2%; Pred. No. 8.7e-30;
Matches 8; Conservative 466; Mismatches 212; Indels 0; Gaps 0;

QY 1 atcgtacataaagtgtgattatcaaatccatthacaactaaatgaaccataat 60
DB 96 www.
QY 61 taaaactaaaaaaccttatacacytacagagagagacatcgtctatag 120
DB 156 www.
QY 121 ttatgatctaacccttcgaaccctcagcagcgtgtgtatgattatcgtact 180
DB 216 www.
QY 181 aatatctgtcttaatactagacacacatgataaacttcgaacacatgtatat 240
DB 276 www.
QY 241 ctatgttgacttaatacctaactaaacagatatagtagatgttatagat 300
DB 336 www.
QY 301 aagtgatgttgactgactgagcctaagtagtagtaagctaaatagtgtgaaact 360
DB 396 www.
QY 361 caaacacccatacaattatagttattttagtaaatagtagtagtatt 420
DB 456 www.
QY 421 tataagctagctttttactagcaatttttaagcacaactaagtttagtatt 480
DB 516 www.
QY 481 tcaaatacccttaagcgttaagtctcttctgaatcttaacgtatgtgagac 540
DB 576 www.
QY 541 aacatttcataagtgactgtttaagtcacgtcagtgataataatttcacatgcg 600
DB 636 www.
QY 601 gtctctaagcaacgcgctgtctaagatattacactagcggtcttaagaagaac 660
QY 661 cgcgcgtgctaagatatctacacta 686
DB 756 www.
RESULT 12
AAFS8255
ID AAF58255 standard; DNA: 938 BP.
XX
AC AAF58255;
XX
DT 24-APR-2001 (first entry)
DE
XX Oligonucleotide D1876.
XX
KM Election-transfer group; ETM; mismatch; genotyping;
XX gene expression; ss.
XX
OS Synthetic.
XX
PN WO200107665-A2.

XX 01-FEB-2001.
PD 26-JUL-2000; 2000MO-US20476.
XX
XX 26-JUL-1999; 9905-0145695.
XX 17-MAR-2000; 2000US-0190259.
XX
XX (CLIN-) CLINICAL MICRO SENSORS INC.
XX
XX UmeK RM;
XX
XX WPI; 2001-159728/16.
XX
XX
XX Nucleic acids containing electron-transfer group, useful as labels in
PT hybridization assays, e.g. for genotyping, allowing repeat analyses on
PT a single surface
XX
XX Example 6; Page 127; 159pp; English.
XX
XX The present invention relates to a composition comprising two nucleic
CC acids each containing an electron-transfer group (ETM) having
CC different redox potentials. The invention is used for electronic
CC detection of nucleic acids, especially of substitutions (mismatches)
CC and single-nucleotide polymorphisms, e.g. for genotyping,
XX monitoring gene expression.
XX
SQ Sequence 938 BP; 4 A; 144 C; 9 G; 5 T; 776 other;
Query Match 12.9%; Score 160.4; DB 22; Length 938;
Best Local Similarity 1.2%; Pred. No. 8.7e-30;
Matches 8; Conservative 466; Mismatches 212; Indels 0; Gaps 0;
QY 1 atcgtacataaagtgtgattatcaaatccatthacaactaaatgaaccataat 60
DB 96 www.
QY 61 taaaactaaaaaaccttatacacytacagagagagacatcgtctatag 120
DB 156 www.
QY 121 ttatgatctaacccttcgaaccctcagcagcgtgtgtatgattatcgtact 180
DB 216 www.
QY 181 aatatctgtcttaatactagacacacatgataaacttcgaacacatgtatat 240
DB 276 www.
QY 241 ctatgttgacttaatacctaactaaacagatatagtagatgttatagat 300
DB 336 www.
QY 301 aagtgatgttgactgactgagcctaagtagtagtaaatagcttgagagaact 360
DB 396 www.
QY 361 caaacacccatacaattatagttattttagtaaatagtagtagtatt 420
DB 456 www.
QY 421 tataagctagctttttactagcaatttttaagcacaactaagtttagtatt 480
DB 516 www.
QY 481 tcaaatacccttaagcgttaagtctcttctgaatcttaacgtatgtgagac 540
DB 576 www.
QY 541 aacatttcataagtgactgtttaagtcacgtcagtgataataatttcacatgcg 600
DB 636 www.

OY 601 gttcttaagcaaccgacgtcctatgatttaccctagcg9gctctaagaac 660
 Db 696 www.
 OY 661 cgcccgctcaagaatttaccacta 686
 Db 756 www. 781

RESULT 13

AA040763/c
 ID AA040763 standard; DNA; 9824 BP.

AA040763;
 AC

14-SEP-1993 (first entry)
 OT

Wild-type shrunken-2 gene.
 DE

Wild-type: shrunken-2; Sh-2; gene; plasmid; replication; Bt-2; starch;
 sequencing; ADP-glucose pyrophosphorylase; ADP-GPP; cloning; sucrose;
 brittle-2; ADP-glucose; pyrophosphate; ATP; sh-2; bt-2; hydrolysis;
 glucose-1-phosphate; chain elongation; starch synthetase; homozygous;
 recessive; supersweet; corn; ss.

Zea mays.
 OS

MO9309237-A.
 PN

13-MAY-1993.
 PD

04-NOV-1992; 92MO-EP02531.
 PF

05-NOV-1991; 91US-0791933.
 PR

(SANO) SANDOZ LTD.
 PA

(SANO) SANDOZ PATENT GMBH.
 PA

(SANO) SANDOZ-ERFINDUNGEN VERW GES MBH.
 PA

Baker FC, Duncan MT, Nichols SE, Pauly MH, Sinibaldi RK;
 PI

Weeks DP;
 PI

WPI; 1993-167702/20.
 DR

Super-sweet corn plants and seed - have sweet or starchy kernels
 at harvest for food or seed, respectively
 XX

Claim 23; Page 30-36; 49pp; English.
 PS

This sequence represents the wild-type shrunken-2 (Sh-2) gene.
 CC The Sh-2 gene contains a sequence which interferes with plasmid
 CC replication which caused difficulties in cloning and sequencing
 CC the Sh-2 gene. The Sh-2 gene encodes a 60 kD protein which is
 CC involved in starch production. The Sh-2 protein represents two
 CC subunits of the four subunit enzyme ADP-glucose pyrophosphorylase
 CC (ADP-GPP). The other two subunits of ADP-GPP comprise a 55 kD
 CC polypeptide encoded by the brittle-2 (Bt-2) gene. ADP-GPP catalyses
 CC the reversible synthesis of ADP-glucose and pyrophosphate from ATP
 CC and glucose-1-phosphate. The reaction is driven by pyrophosphate
 CC hydrolysis. ADP-glucose is the glucosyl donor for starch chain
 CC elongation catalyzed by starch synthetase. When either the Sh-2 or
 CC Bt-2 gene is present in the homozygous recessive state (sh-2 or bt-2
 CC respectively) the 60 kD or 55kD subunits respectively are not
 CC synthesized and little or no functional ADP-GPP is made. Therefore
 CC starch synthesis is impaired, sucrose accumulates to 2-4 times the
 CC levels of normal sweet corn and the result is "supersweet" corn.
 CC

Sequence 9824 BP; 2718 A; 1910 C; 1915 G; 3281 T; 0 other;
 SQ

Query Match 8.7%; Score 108.4; DB 14; Length 9824;
 , Best Local Similarity 75.2%; Pred. No. 9,6e-17;

Matches 152; Conservative 0; Mismatches 41; Indels 9; Gaps 1;
 OY 297 gattaagtgatgattgtaaacctagacctaagtagtaagtaaaattagttg99ga 356
 Db 9541 GACTTAAGGCGGTGTAATGCAATAGACTTAATGTTAGCTGTTAAATTAGCTGAAGA 9482
 OY 357 catcaaaaccacca-----taattatagttatttagtaattgtaataag 407
 Db 9481 CATCTTAACATATAGCTAATTAAGTTCAGCTATTGCTTTTAAACAATTAGCTAATAG 9422
 OY 408 ttagttagtattataagacttaagcttcttttactagcaatttttagccaactaacat 467
 Db 9421 TTAGCTAGCTATTGTTGCTAGCTACTAATTTCACCTCAATTTTGTGCACTAATCTATT 9362
 OY 468 agtttagtgatcaaatacc 489
 Db 9361 AGCTTAATGCTATTAAACAC 9340

RESULT 14

AAV49471/c
 ID AAV49471 standard; CDNA; 4695 BP.

AAV49471;
 AC

10-NOV-1998 (first entry)
 DT

Maize phytase genomic clone p19.14.
 DE

Maize: phytase; PCR; amplification; primer; probe; hybridisation;
 transgenic plant; starch; seed; nutrition; cereal; steep liquor; ss.

Zea mays.
 OS

key Location/Qualifiers
 PR prim_transcript 1935..3403

FT exon /tag= a
 FT 1935..1947

FT exon /tag= b
 FT 1948..2078

FT intron /tag= c
 FT 2079..3403

FT exon /tag= d
 FT 2097..3260

FT CDS /tag= e
 FT /product= "phytase"

FR2751987-A1.
 PM

06-FEB-1998.
 PD

01-AUG-1996; 96FR-0009734.
 PF

01-AUG-1996; 96FR-0009734.
 PR

(BIOC-) BIOCEM SA.
 PA

(INRG) INRA INST NAT RECH AGRONOMIQUE.
 PA

Lescaud AM, Maugest S, Perez P;
 PI

WPI; 1998-133339/13.
 DR

P-PSDB; AAV49696.
 DX

DNA encoding maize phytase enzyme - useful for producing recombinant
 phytase or transgenic plants with increased phytase levels
 XX

Claim 9; Fig 4; 67pp; French.
 PS

This sequence represents the sequence of a genomic clone (p19.14)
 encoding a maize phytase protein. The sequence was isolated from a
 CC

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: December 20, 2001, 11:11:57 ; Search time 89.35 Seconds
(without alignments)
3139,723 Million cell updates/sec

Title: US-09-718-754A-1

Sequence: 1247

1 atcgatacaatgattgatt.....agagtcgatacgaactagca 1247

Scoring table:

IDENTITY NUC
Gapop 10.0, Gapext 1.0

Searched: 351203 seqs, 113238999 residues

Total number of hits satisfying chosen parameters: 702406

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: /cgn2_6/ptodata/2/1na/5A_COMB.seq:*
2: /cgn2_6/ptodata/2/1na/5B_COMB.seq:*
3: /cgn2_6/ptodata/2/1na/5A_COMB.seq:*
4: /cgn2_6/ptodata/2/1na/5B_COMB.seq:*
5: /cgn2_6/ptodata/2/1na/PCPTS_COMB.seq:*
6: /cgn2_6/ptodata/2/1na/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|-------|-------------|--------|-------|--------------------|
| C 1 | 102.6 | 8.2 | 4137 | 3 | US-08-750-357-7 |
| C 2 | 43 | 3.4 | 6768 | 1 | US-08-107-755A-1 |
| C 3 | 43 | 3.4 | 8457 | 1 | US-07-991-667B-1 |
| C 4 | 43 | 3.4 | 8457 | 2 | US-08-544-332-1 |
| C 5 | 42.6 | 3.4 | 7015 | 4 | US-09-177-249-6 |
| C 6 | 42 | 3.4 | 4539 | 1 | US-08-119-512-1 |
| C 7 | 42 | 3.4 | 4539 | 1 | US-08-488-015B-1 |
| C 8 | 42 | 3.4 | 4542 | 3 | US-08-814-412-11 |
| C 9 | 41.4 | 3.3 | 1431 | 4 | US-09-316-083-2 |
| C 10 | 41 | 3.3 | 19124 | 2 | US-08-487-825B-13 |
| C 11 | 40.8 | 3.3 | 10729 | 1 | US-07-781-355-1 |
| C 12 | 40.4 | 3.2 | 615 | 4 | US-08-998-416-186 |
| C 13 | 40.4 | 3.2 | 636 | 4 | US-08-998-416-1137 |
| C 14 | 40.4 | 3.2 | 636 | 4 | US-08-998-416-1137 |
| C 15 | 40.4 | 3.2 | 837 | 4 | US-08-998-416-288 |
| C 16 | 40.4 | 3.2 | 837 | 4 | US-08-998-416-288 |
| C 17 | 39.8 | 3.2 | 2334 | 1 | US-08-062-632-4 |
| C 18 | 39.4 | 3.2 | 3095 | 6 | US-08-998-416-538 |
| C 19 | 38.8 | 3.1 | 828 | 4 | US-08-998-416-538 |
| C 20 | 38.6 | 3.1 | 615 | 4 | US-08-998-416-186 |
| C 21 | 38.6 | 3.1 | 681 | 4 | US-09-299-378-1 |
| C 22 | 38.6 | 3.1 | 3889 | 2 | US-08-648-298-1 |
| C 23 | 38.2 | 3.1 | 837 | 4 | US-08-998-416-288 |
| C 24 | 38 | 3.0 | 3095 | 6 | US-08-998-416-538 |
| C 25 | 37.8 | 3.0 | 724 | 4 | US-08-998-416-683 |
| C 26 | 37.8 | 3.0 | 3528 | 4 | US-08-998-416-683 |
| C 27 | 37.8 | 3.0 | 3528 | 4 | US-08-998-416-683 |

| | | | | | | |
|------|------|-----|------|---|--------------------|--------------------|
| C 28 | 37.8 | 3.0 | 4383 | 6 | 5175095-4 | Patent No. 5175095 |
| C 29 | 37.8 | 3.0 | 4383 | 6 | 5177307-1 | Patent No. 5177307 |
| C 30 | 37.6 | 3.0 | 854 | 4 | US-08-998-416-534 | Sequence 534, App |
| C 31 | 37.2 | 3.0 | 658 | 4 | US-08-998-416-535 | Sequence 535, App |
| C 32 | 37.2 | 3.0 | 711 | 4 | US-08-998-416-786 | Sequence 786, App |
| C 33 | 37.2 | 3.0 | 732 | 4 | US-08-998-416-1036 | Sequence 1036, App |
| C 34 | 37.2 | 3.0 | 828 | 4 | US-08-998-416-538 | Sequence 538, App |
| C 35 | 37.2 | 3.0 | 2435 | 4 | US-09-306-593-1 | Sequence 1, App11 |
| C 36 | 36.8 | 3.0 | 663 | 4 | US-08-998-416-191 | Sequence 191, App |
| C 37 | 36.8 | 3.0 | 860 | 4 | US-08-998-416-287 | Sequence 287, App |
| C 38 | 36.8 | 3.0 | 5852 | 1 | US-07-867-105-2 | Sequence 32, App1 |
| C 39 | 36.6 | 2.9 | 1850 | 3 | US-08-617-860B-32 | Sequence 32, App1 |
| C 40 | 36.6 | 2.9 | 4098 | 2 | US-08-605-105-4 | Sequence 1, App11 |
| C 41 | 36.6 | 2.9 | 6152 | 4 | US-08-973-463-1 | Sequence 191, App |
| C 42 | 36.4 | 2.9 | 663 | 4 | US-08-998-416-191 | Sequence 191, App |
| C 43 | 36.4 | 2.9 | 711 | 4 | US-08-998-416-786 | Sequence 786, App |
| C 44 | 36.4 | 2.9 | 724 | 4 | US-08-998-416-683 | Sequence 683, App |
| C 45 | 36.4 | 2.9 | 732 | 4 | US-08-998-416-1036 | Sequence 1036, App |

ALIGNMENTS

RESULT 1
US-08-750-357-7/c
Sequence 7, Application US/08750357
Patent No. 6008437
GENERAL INFORMATION:
APPLICANT: KREBBERS, ENNO
APPLICANT: WILKINS, MARK
TITLE OF INVENTION: USE OF ANTHOCYANIN GENES TO MAINTAIN
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: BURNS, DONNE, SWECKER & MATHIS, L.L.P.
STREET: P.O. Box 1404
CITY: Alexandria
STATE: Virginia
COUNTRY: United States
ZIP: 22313-1404
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/750,357
FILING DATE: 21-MAR-1997
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: McGowan, Malcolm K.
REGISTRATION NUMBER: 39,300
REFERENCE/DOCKET NUMBER: 018030-100
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 836-6620
TELEFAX: (703) 836-2021
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 4137 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
ORIGINAL SOURCE:
ORGANISM: EcolR-HindIII region of plasmid pCOL13
FEATURE:
NAME/KEY: prim_transcript
LOCATION: 188
FEATURE:
NAME/KEY: exon
LOCATION: 188..212
FEATURE:

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NAME/KEY : -
LOCATION: 4132..4137
OTHER INFORMATION: /label= HindIII
FEATURE:
NAME/KEY : -
LOCATION: 4114..4137
OTHER INFORMATION: /label= polylinker
OTHER INFORMATION: /note= "part of polylinker of pUC19"
US-08-750-35/-7

Query Match      8.2%; Score 102.6; DB 3; Length 4137;
Best Local Similarity 72.2%; Pred.No.3,6e-18;
Matches 151; Conservative 0; Mismatches 49; Indels 9; Gaps 1;

Qy   295  tagataagcggaagtctgaaatcagaacagactaatgtttagtaagctaataatttgttggaa 354
       | | ||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db   3537  ttgcacctaggctggctgttgtaaatacacactgaaactgaaactgaaatgatccctgaaaattggcggaa 3478

Qy   355  gaccatcaaacacccc-----ccaatatcatgatttttagtaaaatttgtttaal 405
       |||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db   3477  gaacatcaaacaataatgacataaataatgatacagataatttacactcttgaaacaataatgacataat 3418

Qy   406  agtatgttagtatatttagtcagagcatttttctcagcaattttttagcaacaaatacaciaa 465
       | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db   3417  atttgcctagcattatttttttacctaacataatttttaataatgtaatttttaaacacacataccta 3358

Qy   466  ttagtttagtgatctcaaatccccctaa 494
       |||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db   3357  ttngttcaagracatttmaacnccctctaa 3329


RESULT          2
US-08-107-755A-1/C
Sequence 1, Application US/08107755A
Patent No.5721352
GENERAL INFORMATION:
APPLICANT: Moyet, Richard W.
APPlicant: Hall, Richard L.
Applicant: Grudl, Michael E.
TITLE OF INVENTION: No. 5721352el Entomopoxvirus Expression System
NUMBER OF SEQUENCES: 40
CORRESPONDENCE ADDRESS:
ADDRESSER: David R. Saliwanchik
STREET: 2421 N.W. 41st Street, Suite A-1
CITY: Gainesville
STATE: Florida
COUNTRY: U.S.A.
ZIP: 32606
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/107,755A
FILING DATE: 19-AUG-1993
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/827,658
FILING DATE: 30-JAN-1992
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 07/657,584
FILING DATE: 19-FEB-1991
ATTORNEY/AGENT INFORMATION:
NAME: Saliwanchik, David R.
REGISTRATION NUMBER: 51,794
REFERENCE/DOCKET NUMBER: UF114,C2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (904) 375-8100
TELEFAX: (904) 372-5800
SEQUENCE CHARACTERISTICS:

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; LENGTH: 6768 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: unknown
; MOLECULE TYPE: DNA (genomic)
; ORIGINAL SOURCE:
; ORGANISM: Amsacta moorei entomopoxvirus
; FEATURE:
; NAME/KEY: CDS
; LOCATION: complement (65..1459)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1474..2151
; FEATURE:
; NAME/KEY: CDS
; LOCATION: complement (2239..2475)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 2502..2987
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 3080..6091
; NAME/KEY: CDS
; LOCATION: complement (6277..6768)
; US-08-107-755A-1

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Query Match          3.4%; Score 43; DB 1: Length 6768;
Best Local Similarity 47.8%; Pred. No. 0.044;
Matches 187; Conservative 0; Mismatches 200; Indels 4; Gaps 2;

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OY 145 aaccatcagcagtggtgagtgtaagttactgatactatctgtcttaactcaga 204
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 2315 AACCATCTACTGATGATGTTGGGAGATTAACCTTTAGAGGTAAATTTACTCTAAA 2256
OY 205 ccaactgataatactcttcgacacacatgatactatctatctgtgacttaatact 264
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DB 2255 GCNAAAAAATAAAGACTGTAAATGATTAATTAATGACATAATATATATTT 2196
OY 265 aaatccaagatattagtagagatgttagtatagatgaagtgatgttgaatgcactaga 324
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 2195 TTATTCATTTTAAATAAATAATGTTAGTATTTACTTAATATTAATGATTTATGACA 2136
OY 325 gctaatagttagtgaataaattagttgagacatccaacacccataactaattagtt 384
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 2135 AAAAGTGTCTCGATGATTTTAAATGATATTTATGAGTTAATTTATTCATTAAT 2076
OY 385 attc-cttagtaattagttatagtttagtttagttatataagccttttttacta 442
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DB 2075 CTCACATTTAGTTTAAATAGCAAAATTTTAAATATTAATTAATAGATATATTTATTT 2016
OY 443 gcaatttttttagccaactaactaattagtttagttatccaataaccctaagccgttaa 502
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 2015 ACGGATTTTCTCTCATTAATTACATA--TTATATATATCTAGATTTCATAAATTCATAT 1958
OY 503 gtgatgtctcttctagaacttaaccgtaag 533
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 1957 GTGATACTATATCTAATATACATCATATTTTG 1927

```

```

RESULT 3
US-07-991-867B-1/c
; Sequence 1, Application US/07991867B
; Patent No. 5476781
; GENERAL INFORMATION:
; APPLICANT: Moyer, Richard W.
; APPLICANT: Hall, Richard L.
; APPLICANT: Gruhl, Michael E.
; TITLE OF INVENTION: No. 5476781el Entomopoxvirus Expression System
; NUMBER OF SEQUENCES: 66
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: David R. Saliwanchik

```

```

; STREET: 2421 N.W. 41st Street, Suite A-1
; CITY: Gainesville
; STATE: FL
; COUNTRY: USA
; ZIP: 32606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/991,867B
; FILING DATE: 12-DEC-1992
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO 92/14818
; FILING DATE: 12-FEB-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/827,685
; FILING DATE: 30-JAN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/657,584
; FILING DATE: 19-FEB-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Saliwanchik, David R.
; REGISTRATION NUMBER: 31,794
; REFERENCE/DOCKET NUMBER: UFI14.C3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 904-375-8100
; TELEFAX: 904-372-5800
; INFORMATION FOR SRO ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8457 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: unknown
; MOLECULE TYPE: DNA (genomic)
; ORIGINAL SOURCE:
; ORGANISM: Amsacta moorei entomopoxvirus
; FEATURE:
; NAME/KEY: CDS
; LOCATION: complement (65..1459)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1474..2151
; FEATURE:
; NAME/KEY: CDS
; LOCATION: complement (2239..2475)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 2502..2987
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 3080..6091
; NAME/KEY: CDS
; LOCATION: complement (6277..6768)
; US-07-991-867B-1

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Query Match          3.4%; Score 43; DB 1: Length 8457;
Best Local Similarity 47.8%; Pred. No. 0.048;
Matches 187; Conservative 0; Mismatches 200; Indels 4; Gaps 2;
OY 145 aaccatcagcagtggtgagtgtaagttactgatactatctgtcttaactcaga 204
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 2315 AACCATCTACTGATGATGTTGGGAGATTAACCTTTAGAGGTAAATTTACTCTAAA 2256
OY 205 ccaactgataatactcttcgacacacatgatactatctatctgttgacttaactact 264
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 2255 GCNAAAAAATAAAGACTGTAAATGATTAATTAATTAATGACATAATATATATTT 2196
OY 265 aaatccaagatattagtagagatgttagtatagatgaagtgatgttgaatgcactaga 324

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; MEDIUM TYPE: floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: ASCII (text)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/488,015B
; FILING DATE: 07-JUN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Vincent, Matthew P.
; REGISTRATION NUMBER: 36,709
; REFERENCE/DOCKET NUMBER: H0V-008.02
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 832-1000
; TELEFAX: (617) 832-7000
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4539 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: both
; MOLECULE TYPE: other nucleic acid
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 969..1259
; OTHER INFORMATION: /product= "E3 exon"
; NAME/KEY: misc_feature
; LOCATION: 1290..1559
; OTHER INFORMATION: /product= "E5 exon"
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US-08-488-015B-1

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Query Match          3.4%; Score 42; DB 1; Length 4539;
Best Local Similarity 47.5%; Pred. No. 0.07;
Matches 155; Conservative 0; Mismatches 170; Indels 1; Gaps 1;

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Qy 20 tatcaatattccattacacctaataagaaacaaatatttaaaacaaacaaacac 79
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Db 1822 TATTCATTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTTA 1881
Qy 80 ttataccgtaacagagagagagagagagagagagagagagagagagagagag 139
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1882 TGTATTGGAAATGACATACATCATATATACCATTTAGTATATATTTGAGACTA 1941
Qy 140 ctctgaaccatcagcagtggtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 199
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Db 1942 AGTTAGATATTTACGATTTTATGATTAACAGATTAACCCATGATAATTTATTTATTTAA 2001
Qy 200 tagcaccacatgataataatcttcgaacacacatgatatatctatctgtgacttaac 259
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 2002 TAATTAATAAATAATTAATAT-ACCAATATATATATTTATTTATTTATTTATTTATTTA 2060
Qy 260 ataactaaatccaagatatagtagagagagagagagagagagagagagagagag 319
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 2061 ATAAATTTTATATATATATTAATAATTTATTTGATTAAGAAATATATTTTATAGAA 2120
Qy 320 cttagagctaagtagtagtagtagtagtagtagtagtagtagtagtagtagtag 345
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Db 2121 ATTTCTTTATTTATTTAGAGGCTAATA 2146

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RESULT 8
US-08-814-412-11
; Sequence 11, Application US/08814412
; Patent No. 6150141
; GENERAL INFORMATION:
; APPLICANT: Jarrell Ph.D., Kevin A.
; TITLE OF INVENTION: Intron-Mediated Techniques and Reagents
; NUMBER OF SEQUENCES: 46
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Choate, Hall & Stewart
; STREET: 53 State Street
; CITY: Boston

```

```

;
; STATE: MA
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/814,412
; FILING DATE: 11-MAR-1997
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Jarrell Ph.D., Brenda H.
; REGISTRATION NUMBER: 39,223
; REFERENCE/DOCKET NUMBER: 0079571-0040
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617 248 5000
; TELEFAX: 617 248 4000
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4542 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: circular
; MOLECULE TYPE: other nucleic acid
; DESCRIPTION: /desc = "plasmid DNA"
; IMMEDIATE SOURCE:
; CLONE: pINVT1
;
US-08-814-412-11

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Query Match          3.4%; Score 42; DB 3; Length 4542;
Best Local Similarity 47.5%; Pred. No. 0.07;
Matches 155; Conservative 0; Mismatches 170; Indels 1; Gaps 1;

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Qy 20 tatcaatattccattacacctaataagaaacaaatatttaaaacaaacaaacac 79
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Db 1825 TATTCATTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTTA 1884
Qy 80 ttataccgtaacagagagagagagagagagagagagagagagagagagagag 139
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1885 TGTATTGGAAATGACATACATCATATATACCATTTAGTATATATTTGAGACTA 1944
Qy 140 ctctgaaccatcagcagtggtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 199
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1945 AGTTAGATATTTACGATTTTATGATTAACAGATTAACCCATGATAATTTATTTATTTAA 2004
Qy 200 tagcaccacatgataataatcttcgaacacacatgatatatctatctgtgacttaac 259
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 2005 TAATTAATAAATAATTAATAT-ACCAATATATATATTTATTTATTTATTTATTTATTTA 2063
Qy 260 ataactaaatccaagatatagtagagagagagagagagagagagagagagagag 319
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 2064 ATAAATTTTATATATATATTAATAATTTATTTGATTAAGAAATATATTTTATAGAA 2123
Qy 320 cttagagctaagtagtagtagtagtagtagtagtagtagtagtagtagtagtag 345
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 2124 ATTTCTTTATTTATTTAGAGGCTAATA 2149

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RESULT 9
US-09-316-083-2
; Sequence 2, Application US/09316083A
; Patent No. 6280942
; GENERAL INFORMATION:
; APPLICANT: The Institute of Physical and Chemical Research
; TITLE OF INVENTION: Endonuclease
; FILE REFERENCE: PH-651
; CURRENT APPLICATION NUMBER: US/09/316,083A
; CURRENT FILING DATE: 1999-05-20
; EARLIER APPLICATION NUMBER: JP98/141861
; EARLIER FILING DATE: 1998-05-22

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APPLICATION NUMBER: CH 0016/97
FILING DATE: 31-DEC-1996
ATTORNEY/AGENT INFORMATION:
NAME: Meigs, J. Timothy
REGISTRATION NUMBER: 38, 241
REFERENCE/DOC/ENT NUMBER: PF-5-30306/A/CGCL976
TELECOMMUNICATION INFORMATION:
TELEPHONE: 919-541-8587
TELEFAX: 919-541-8689
INFORMATION FOR SEQ ID NO: 186:
SEQUENCE CHARACTERISTICS:
LENGTH: 615 base pairs
TYPE: nucleic acid

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.3
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/998,416
FILING DATE: 24-DEC-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: CH 0016/97
FILING DATE: 31-DEC-1996
ATTORNEY/AGENT INFORMATION:
NAME: Weigs, J. Timothy

Fri Dec 21 09:04:54 2001

us-09-718-754a-1.rni

Page 10

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1 Sequence 288, Application US/08998416
2 Patent No. 6239264
3
4 GENERAL INFORMATION:
5 APPLICANT:      Philippsen, Peter
6 APPLICANT:      Pohlmann, Rainer
7 APPLICANT:      Steiner, Sabine
8 APPLICANT:      Mohr, Christine
9 APPLICANT:      Wendland, Jürgen
10 APPLICANT:      Knechtle, Philipp
11 APPLICANT:      Reibischung, Corinne
12 TITLE OF INVENTION:  GENOMIC DNA SEQUENCES OF ASHBYA GOSSETII
13 NUMBER OF SEQUENCES: 1152
14
15 CORRESPONDENCE ADDRESS:
16 ADDRESSEE:      No. 6239264artis Corporation
17 STREET:          3054 Cornwallis Road
18 CITY:            Research Triangle Park
19 STATE:           No. 6239264th Carolina
20 COUNTRY:         USA
21 ZIP:             27709
22
23 COMPUTER READABLE FORM:
24 MEDIUM TYPE:    floppy disk
25 COMPUTER:        IBM PC compatible
26 OPERATING SYSTEM: PC-DOS/MS-DOS
27 SOFTWARE:        Patentin Release #1.0, Version #1.30
28
29 CURRENT APPLICATION DATA:
30 APPLICATION NUMBER: US/08/998,416
31 FILING DATE:     24-DEC-1997
32 CLASSIFICATION:  435
33
34 PRIOR APPLICATION DATA:
35 APPLICATION NUMBER: CH 0016/97
36 FILING DATE:     31-DEC-1996
37 ATTORNEY/AGENT INFORMATION:
38 NAME:           Weigs, J. Timothy
39 REGISTRATION NUMBER: 38, 241
40 REFERENCE/DOCKET NUMBER: PF/5-30306/A/CGC1976
41 TELECOMMUNICATION INFORMATION:
42 TELEPHONE:       919-541-8587
43 TELEFAX:         919-541-8689
44 INFORMATION FOR SEQ ID NO: 288:
45 SEQUENCE CHARACTERISTICS:
46 LENGTH:         837 base pairs
47 TYPE:            nucleic acid
48 STRANDEDNESS:   single
49 TOPOLOGY:        linear
50 MOLECULE TYPE:   DNA (genomic)
51 ORIGINAL SOURCE:
52 ORGANISM:        PAG1241RP
53
54 US-08-998-416-288

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| | | 3.28; Score 40.4; DB 4; Length 837; |
| | Query Match | 47.38; Pident No. 0.094; |
| | Best Local Similarity | Matches 157; Conservative 0; Mismatches 171; Indels 4; Gaps 1 |
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| Dd | 45 tttttattatattatttttgaatttttatttttgaacattattatttcattttttttaa | 104 |
| Oy | 220 cttcgaacacatctatactcatctgttgaccttaactcaactcaacagatata | 279 |
| Dd | 105 ttattattttgatatttttatttactttattattttatttttttttttttttttttt | 164 |
| Oy | 280 gttagagatcttagatagatttagagtgatgctttagatgacactgagctaaatgattag | 339 |
| Dd | 165 tttttatt | 224 |
| Oy | 340 cttaaatctagcttgagacattcaacacacctcaactcatctatctagttcttttagttaaata | 399 |
| Dd | 225 ttcatt | 284 |
| Oy | 400 gttaaatctagcttagtcttattcaataagcttagctttt---ttactagcaacttttagc | 455 |

Db 285 TAAATGATATTCATCAATTAATTAATTAATTTATTAATGTTATTAATAAATAATATT 344
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 Db 345 TTATATTATTAAAGATTATTTATTTAAATA 376

Search completed: December 20, 2001, 12:16:39
Job time: 3882 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: December 20, 2001, 10:01:26 : Search time 1550.78 seconds
(without alignments)
8640.804 Million cell updates/sec

Title: US-09-718-754A-1

Sequence: 1 atcgatacaaatgattgacatt.....agagtcgatacactagca 1247

Scoring table: IDENTITY_NUC
Gapop 10.0, Capext 1.0

Searched: 11351937 seqs, 5372889281 residues

Total number of hits satisfying chosen parameters: 22703874

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database:

Listing first 45 summaries

EST:
1: em_estfun:
2: em_esthm:
3: em_estin:
4: em_estov:
5: em_estpl:
6: em_estda:
7: em_estro:
8: em_estov:
9: em_hic:
10: qb_est1:
11: qb_est2:
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16: em_gss_inv:
17: em_gss_pln:
18: em_gss_pro:
19: em_gss_rpd:
20: em_gss_vrt:
21: em_gss_other:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|-------|-------------|--------|-------|-------------|
| 1 | 126.6 | 10.2 | 365 | 10 | A1619399 |
| 2 | 126.6 | 10.2 | 407 | 10 | A1657360 |
| 3 | 118.6 | 9.5 | 687 | 10 | AM066683 |
| 4 | 93.8 | 7.5 | 616 | 10 | AM147120 |
| 5 | 93.8 | 7.5 | 620 | 11 | BF727815 |
| 6 | 86.8 | 7.0 | 497 | 10 | AM258129 |
| 7 | 76 | 6.1 | 474 | 13 | BH130093 |
| 8 | 76 | 6.1 | 1101 | 13 | CNS00EVL |
| 9 | 67.8 | 5.4 | 412 | 10 | BE510052 |
| 10 | 65.6 | 5.3 | 1101 | 13 | CNS00L72 |
| 11 | 64.6 | 5.2 | 438 | 13 | AQ844669 |
| 12 | 63.6 | 5.1 | 1101 | 13 | CNS003BB |

| | | | | | | |
|------|------|-----|------|----|-----------|----------------------|
| C 13 | 63.4 | 5.1 | 1101 | 13 | CNS00EVL | AL069706 Drosophila |
| C 14 | 63.2 | 5.1 | 928 | 13 | CNS00DKY | AL071865 Drosophila |
| C 15 | 61.6 | 4.9 | 928 | 13 | CNS00DKY | AL071865 Drosophila |
| C 16 | 61.4 | 4.9 | 192 | 10 | A1612358 | A1612358 486079H11 |
| C 17 | 61.4 | 4.9 | 1125 | 10 | AL547503 | AL547503 AL547503 |
| C 18 | 61.2 | 4.9 | 1027 | 13 | CNS02PT50 | AL212733 Tetradodon |
| C 19 | 60.8 | 4.9 | 550 | 10 | A1600397 | AL1600397 486071A03 |
| C 20 | 60.8 | 4.9 | 1101 | 13 | CNS0039C | AL1603921 Drosophila |
| C 21 | 59.6 | 4.8 | 1496 | 13 | BH127174 | BH127174 G-10J3 |
| C 22 | 57.4 | 4.6 | 1101 | 13 | CNS0039C | AL063921 Drosophila |
| C 23 | 56.4 | 4.5 | 836 | 13 | CNS01100 | AL069440 Drosophila |
| C 24 | 56.4 | 4.5 | 1101 | 13 | CNS00E07 | AL069440 Drosophila |
| C 25 | 56.2 | 4.5 | 894 | 13 | BH136681 | BH136681 ENTOR72TF |
| C 26 | 55.4 | 4.4 | 773 | 11 | BG584434 | BG584434 1024040A0 |
| C 27 | 55.2 | 4.4 | 758 | 10 | AV756150 | AV756150 AV756150 |
| C 28 | 55.2 | 4.4 | 1001 | 13 | CNS0155H | AL105023 Drosophila |
| C 29 | 54.8 | 4.4 | 1190 | 13 | CNS020N7 | AL206908 Tetradodon |
| C 30 | 54.6 | 4.4 | 994 | 13 | CNS04NOJ | AL298972 Tetradodon |
| C 31 | 54.6 | 4.4 | 1092 | 13 | CNS020K7 | AL175686 Tetradodon |
| C 32 | 54.4 | 4.4 | 1101 | 13 | CNS0021J | AL1061936 Drosophila |
| C 33 | 54.4 | 4.4 | 1225 | 13 | CNS0161D | AL106171 Drosophila |
| C 34 | 54.2 | 4.3 | 796 | 10 | AV704385 | AV704385 AV704385 |
| C 35 | 53.8 | 4.3 | 1086 | 13 | CNS007KX | AL069682 Drosophila |
| C 36 | 53.6 | 4.3 | 1101 | 13 | CNS00L72 | AL078714 Drosophila |
| C 37 | 53.6 | 4.3 | 1161 | 13 | CNS073Y8 | AL042818 clone BA0 |
| C 38 | 53.6 | 4.3 | 1201 | 13 | CNS0167M | AL106336 Drosophila |
| C 39 | 53.4 | 4.3 | 876 | 13 | CNS005G1 | AL053529 Drosophila |
| C 40 | 53.2 | 4.3 | 619 | 11 | BF296544 | BF296544 038B2E2 |
| C 41 | 53.2 | 4.3 | 987 | 13 | CNS014PO | AL104456 Drosophila |
| C 42 | 53 | 4.3 | 994 | 13 | CNS04NOJ | AL298972 Tetradodon |
| C 43 | 52.8 | 4.2 | 1085 | 13 | CNS016YR | AL107373 Drosophila |
| C 44 | 52.8 | 4.2 | 1101 | 13 | CNS0022U | AL0977152 Drosophila |
| C 45 | 52.6 | 4.2 | 139 | 13 | A2916538 | A2916538 PstI_7_c4 |

ALIGNMENTS

RESULT 1
A1619399/c 365 bp mRNA EST 21-APR-1999
LOCUS 486093G11.x1 486 - leaf primordia CDNA library from Hake lab Zea
DEFINITION mays cDNA, mRNA sequence.
ACCESSION A1619399
VERSION A1619399.1 GI:4628525
KEYWORDS EST.
SOURCE Zea mays.
ORGANISM Zea mays.
REFERENCE Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC
clade: Panicoideae; Andropogoneae; Zea.
REFERENCE 1 (bases 1 to 365)
AUTHORS Walbot V.
TITLE maize ESTs from various CDNA libraries sequenced at Stanford
COMMENT
JOURNAL Unpublished (1999)
CONTACT: Walbot V
DEPARTMENT: Department of Biological Sciences
STANFORD UNIVERSITY
855 California Ave, Palo Alto, CA 94304, USA
TEL: 650 723 2227
FAX: 650 725 8221
EMAIL: walbot@stanford.edu
PLATE: 486093 row: G column: 11.
LOCATION/Qualifiers
1. 365
/organism="Zea mays"
/cultivar="B73"
/db_xref="taxon:4577"
/clone_id="486 - leaf primordia CDNA library from Hake
lab"
/tissue_type="leaf primordia"
/dev_stage="p7-p11 leaf"

Page 3

RESULT 5

| | | |
|----------|------------|------------|
| VERSION | AW258129.1 | GI:6626597 |
| KEYWORDS | EST. | |
| SOURCE | Zee mays. | |

ORGANISM *Zea mays*

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Focaceae; PACC
clade; Panicoideae; Andropogoneae; Zea.

REFERENCE

Walbot, V.

TITLE

Malze ESI3 11011 Val
University

FEATURES

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source
1. .1107
/organism="Drosophila melanogaster"
/db_xref="taxon:7227"
/clone_id="RpCI-98"
/clone="BACR29823"
/note="end : T7"

BASE COUNT      419 a      91 c      60 g      259 t      232 others
ORIGIN

```

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Query Match      6.1%; Score 76; DB 13; Length 1101;
Best Local Similarity 34.7%; Pred. NO. 1.9e-05;
Matches 163; Conservative 81; Mismatches 226; Indels 0; Gaps 0;

```

[illegible]

| | |
|----------------|--|
| RESULT | /9 |
| LOCUS | BE510052/c |
| DEFINITION | BE510052 412 bp mRNA EST 07-AUG-2000 946018G10.x1 946 - tassal primordium prepared by Schmidt lab Zea |
| ACCESSION | mays cDNA, mRNA sequence. |
| VERSION | BE510052 |
| KEYWORDS | BE510052.1 GI:97313100 |
| SOURCE | EST. |
| ORGANISM | Zea mays. |
| Eukaryote: | Eukaryotes; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta |
| SpERMatophyta: | Magnoliophyta; Liliopsida; Poales; Poaceae; PACC |
| Clade: | Panicoidae; Andropogoneae; Zea. |
| REFERENCE | 1 (bases 1 to 412) |
| AUTHORS | Walboe,V. |
| TITLE | Maize ESTs from various cDNA libraries sequenced at Stanford University |

JOURNAL
COMMENT

Unpublished (1999)
Contact: Walbot V
Department of Biological Sciences
Stanford University
855 California Ave, Palo Alto, CA 94304, USA
Tel: 650 723 2227
Fax: 650 723 8221
Email: walbot@stanford.edu
Plate: 946019 row: G, column: 10.

FEATURES
SOURCE

```

/organism="zea mays"
/cultivar="OH43"
/db_xref="taxon:4577"
/cclone_1lb="946 - tassels primordium prepared by Schmidt
1ab"
/tissue_type="tassels"
/dev_stage="just after the transition from vegetative to
inflorescence development"
/lab_host="XLOLR"
/notes="Organ: tassels; Vector: HybridZAP; Site_1: EcoRI;
Site_2: XhoI; George Chuck dissected immature tassels
between 1mm and 3mm. Sharon Stanfield prepared the cDNA
library in HybridZAP. Sample insert size range was 350 bp
to 3 kb with a 1 kb average."

```

| | | | | |
|-----------------------|--------|--------------------|--------|-------------|
| Query Match | 5.48; | Score 67.8; | DB 10; | Length 412; |
| Best Local Similarity | 72.78; | Pred. No. 0.00097; | | |

| | | | | | | | | | | |
|----|---------|---|--------------|----|------------|-----|--------|----|------|---|
| | Matches | 117; | Conservative | 0; | Mismatches | 37; | Indels | 7; | Gaps | 2 |
| QY | 287 | tgttaagtaaaggatgatttgaatgcacgaagggcgaataagttagtacaatat | 346 | | | | | | | |
| Db | 159 | TGCTGTAGATTAAATATTTTTGCTGTTTTGCATTGCACATGACG--CAAGTAGCGTCGTAATAAT | 102 | | | | | | | |
| OY | 347 | tacttgagaacattcaaacacctatacat-----tatagtattttttaagaatttgt | 401 | | | | | | | |
| Db | 101 | TACTGTAAACAACCAACCATMTAATCTGTGTAGCATTAATACCTAAATTTTGGCATAATTGAC | 42 | | | | | | | |
| OY | 402 | taaatagtagttagtattattataagctagctcttttctaacta | 442 | | | | | | | |
| Db | 41 | TAAACAATTAGCTAGTATTATTGTTAGTAGCTATTATTATTTGTA | 1 | | | | | | | |

RESULT 10

| LOCUS | LOCUS | LOCUS | LOCUS |
|--|---------|-------|-------------|
| CNS000172 | 1101 bp | DNA | GSS |
| Drosophila melanogaster genome survey sequence | | | 14-JUN-1999 |
| DEFINITION | | | |
| BAC44819 of RGL-98 library from <i>Drosophila melanogaster</i> (fruit fly), genomic survey sequence. | | | |

| | |
|-----------|--------------------------------|
| ACCESSION | AL078714 |
| VERSION | AL078714.1 |
| KEYWORDS | GI:5102004 |
| SOURCE | GSS. |
| ORGANISM | fruit fly. |
| | <i>Drosophila melanogaster</i> |

REFERENCE
1 (bases 1 to 1101)

TITLE Direct Submission
JOURNAL Genoscope - Centre National de Séquençage
Submitted (11-JUN-1999) Genoscope - Centre National de Séquençage
BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
Web : www.genoscope.cns.fr)
COMMENT Determination of this BAC-end sequence was carried out as part of a

The BDGP is constructing a physical map of the *Drosophila melanogaster* genome using these BACs. For further information please see <http://www.fruitfly.org> The BDGP *Drosophila* melanogaster BAC library was prepared by Kazuhiro Oosawa and Aaron Mammoser. In Pletzer de Jong's laboratory in the Department of

Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPCI-98 and was constructed by partial EcoRI digestion of Drosophila DNA provided by the BDGP from the isogenic strain Y2; on bw sp, the same strain used for the BDGP's P1 and EST libraries. A more detailed description of the library and how to order individual BAC clones, the entire library, or filters for hybridization from the BACPAC Resource Center can be found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.

FEATURES

Location/Qualifiers
 1. 1101
 /organism="Drosophila melanogaster"
 /db_xref="taxon:7227"
 /clone_lib="RPCI-98"
 /clone="BACR48P19"
 /note="end : rev3"
 BASE COUNT 469 a 6 c 69 g 151 t 406 others
 ORIGIN

Query Match 5.3%; Score 65.6; DB 13; Length 1101;
 Best Local Similarity 30.7%; Pred. No. 0.0022;
 Matches 185; Conservative 114; Mismatches 303; Indels 0; Gaps 0;

OY 6 acataaagtgtgataacataatccattacaactaataagaacaaatttaataa 65
 DB 257 AA 316
 OY 66 aactaaaaaaccttaccgcgtacagagagagagcactgctatattttaa 125
 DB 317 AA 376
 OY 126 tgcatttaaacacccttcacacatcagcagtggtgtagttagttagttagt 185
 DB 377 AA 436
 OY 186 ctgtcttactaactagcaccacgtatataactcttcgacacacgttatctat 245
 DB 437 AA 496
 OY 246 gtgtgacttaatacactaatacccaagatattagtagagattgttagtaagt 305
 DB 497 TTTTATTTTWTATTTTAAADDBWAAWMTTATTTTWTATTTTATTTTWTWK 556
 OY 306 gactgttaagtcactagcactaataagtagtagtaataactgctgagacatcaaac 365
 DB 557 ATTTDTTKKAKYAAKTAAMAAWMTTATTTTATTTTATTTTAKTKWAKWAMDIATTT 616
 OY 366 accctataatattagttatttttagtaataattagtagtagtagttagtatttaa 425
 DB 617 TTTTATTTTWTATTTTAAATTTTWTATTTTATTTTATTTTATTTTATTTTATTTA 676
 OY 426 gctagcttttttactagcaatttttagcacaactaataattagtttagtgcacaa 485
 DB 677 AATTAATAAAWTTTDTTAAWMTTATTTTATTTTATTTTATTTTATTTTATTTTATTT 736
 OY 486 taaccttaagccgttaagtagagctcttcctcagaactcaacgttatgtaggagaacaaat 545
 DB 737 WAAADKKKGGKGGKGGKGGKGGKGGKGGKGGKGGKGGKGGKGGKGGKGGKGGKGGKGGK 796
 OY 546 ttcataaggtgactgtttaaagtcacgcagtgataataatttccatgcggtttc 605
 DB 797 KKAATTTTGGKGGKGGKGGKGGKGGKGGKGGKGGKGGKGGKGGKGGKGGKGGKGGKGGK 856
 OY 606 tt 607
 DB 857 TT 858

RESULT 11
 A0844669 438 bp DNA GSS 03-JUN-1999
 LOCUS A0844669/c
 DEFINITION anaf03 JM107 filtered library Zea mays genomic. DNA sequence.
 ACCESSION A0844669

VERSION A0844669.1 GI:6203157
 KEYWORDS GSS.
 SOURCE Zea mays.
 ORGANISM Zea mays.

REFERENCE
 AUTHORS Stein, L., McCombie, W.R. and Martienssen, R.A.
 TITLE Differential methylation of genes and retrotransposons allows
 JOURNAL Nat. Genet. 23, 305-308 (1999)
 COMMENT Contact: Martienssen RA
 Cold Spring Harbor Laboratory
 1 Bungtown Rd., Cold Spring Harbor, NY 11724, USA
 Tel: 516 367 8322
 Fax: 516 367 8369
 Email: martienss@cshl.org
 Seq primer: forward
 Class: Shotgun.

FEATURES

source

Location/Qualifiers
 1. 438
 /organism="Zea mays"
 /cultivar="B73"
 /db_xref="taxon:4577"
 /clone_lib="JM107 filtered library"
 /note="Organ: Immature ears; Vector: M13; Site: 1; Xba I;
 DNA prepared from purified nuclei was digested with the
 methylation insensitive enzyme Spe I, size fractionated to
 enrich for the 0.5 to 4 kbp fraction, ligated into Xba I
 digested M13 vector and electroporated into E.coli JM107."
 BASE COUNT 63 a 138 c 128 g 108 t 1 others
 ORIGIN

Query Match 5.2%; Score 64.6; DB 13; Length 438;
 Best Local Similarity 83.9%; Pred. No. 0.0041;
 Matches 73; Conservative 0; Mismatches 14; Indels 0; Gaps 0;

OY 294 atagattaaagtgttgaatgactagactaataagtagtagtagtaataattgag 353
 DB 91 ATACTTAAGAAAGAGTGTGATGACTAGAGCTAATAGTGTAGCTAAATAGTACTG 32
 OY 354 agacattcaaacacccatcaattatc 380
 DB 31 AGACATCCAAACCACTAGCTAATATT 5

RESULT 12
 A0844669 1101 bp DNA GSS 03-JUN-1999
 LOCUS A0844669/c
 DEFINITION Drosophila melanogaster genome survey sequence T7 end of BAC #
 BACR08608 of RPCI-98 library from Drosophila melanogaster (fruit
 fly) genomic survey sequence.
 ACCESSION A0844669
 VERSION A0844669.1 GI:4941845
 KEYWORDS GSS.
 SOURCE fruit fly.
 ORGANISM Drosophila melanogaster.

REFERENCE
 AUTHORS Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
 Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
 Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
 TITLE 1 (bases 1 to 1101)
 JOURNAL Direct Submission
 Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage :
 BP 191 91006 Evry cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
 - Web : www.genoscope.cns.fr)
 Determination of this BAC end sequence was carried out as part of a
 collaboration with the Berkeley Drosophila Genome Project (BDGP).
 The BDGP is constructing a physical map of the Drosophila

COMMENT

Fri, Dec 21 09:04:55 2001

us-09-718-754a-1.rst

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[illegible]

Search completed: December 20, 2001, 11:40:55
Job time: 5969 sec